

SEQUENCE LISTING

<110> APPLICANT: Geiser, Martin  
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Raulf, Friedrich  
Zenke, Gerhard

<120> TITLE: ATOMIC STRUCTURE OF THE CATALYTIC DOMAIN  
FOR USE IN DESIGNING AND IDENTIFYING INHIBITORS OF ZAP-70  
KINASE

<130> DOCKET/FILE REFERENCE: 4-32688A

<140> CURRENT APPLICATION NUMBER: US10/528,709  
<141> FILING DATE: 2003-09-25

<150> PRIOR APPLICATION NUMBER: PCT/EP03/10686  
<151> FILING DATE: 2003-09-25

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<151> FILING DATE: 2002-09-26

<160> NUMBER OF SEQUENCES: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO:1  
<211> LENGTH: 619  
<212> TYPE: PRT  
<213> ORGANISM:Homo sapiens

<400> SEQ ID NO:1  
Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser  
1 5 10 15  
Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly  
20 25 30  
Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu  
35 40 45  
Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln  
50 55 60  
Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro  
65 70 75 80  
Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys  
85 90 95  
Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro  
100 105 110  
Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg  
115 120 125  
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser  
130 135 140  
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg  
145 150 155 160  
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys

165	170	175													
Leu	Tyr	Ser	Gly	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg
180								185					190		
Lys	Glu	Gln	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val
195							200					205			
Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro
210						215					220				
Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys
225					230					235			240		
Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn
						245			250				255		
Ser	Ser	Ala	Ser	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala
						260			265			270			
His	Pro	Ser	Thr	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn
						275			280			285			
Ser	Asp	Gly	Tyr	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys
						290			295			300			
Pro	Arg	Pro	Met	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser
						305			310			315			320
Asp	Pro	Glu	Glu	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn
						325				330			335		
Leu	Leu	Ile	Ala	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val
						340			345			350			
Arg	Gln	Gly	Val	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile
						355			360			365			
Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met	Met
						370			375			380			
Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val	Arg
						385			390			395			400
Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu	Met
						405				410			415		
Ala	Gly	Gly	Gly	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu	Glu
						420			425			430			
Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly
						435			440			445			
Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala
						450			455			460			
Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp	Phe
						465			470			475			480
Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg
						485			490			495			
Ser	Ala	Gly	Lys	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn
						500			505			510			
Phe	Arg	Lys	Phe	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr
						515			520			525			
Met	Trp	Glu	Ala	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met	Lys
						530			535			540			
Gly	Pro	Glu	Val	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu	Cys
						545			550			555			560
Pro	Pro	Glu	Cys	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys	Trp
						565				570			575		
Ile	Tyr	Lys	Trp	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln	Arg
						580			585			590			
Met	Arg	Ala	Cys	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro	Pro
						595			600			605			
Gly	Ser	Thr	Gln	Lys	Ala	Glu	Ala	Ala	Cys	Ala					
						610			615						

<210> SEQ ID NO:2  
<211> LENGTH: 322  
<212> TYPE: PRT  
<213> ORGANISM:Homo sapiens

<400> SEQ ID NO:2  
Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met Asp Thr Ser  
1 5 10 15  
Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys  
20 25 30  
Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly  
35 40 45  
Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys  
50 55 60  
Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys  
65 70 75 80  
Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu  
85 90 95  
Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala  
100 105 110  
Leu Met Leu Val Met Glu Met Ala Gly Gly Pro Leu His Lys Phe  
115 120 125  
Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu  
130 135 140  
Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe  
145 150 155 160  
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His  
165 170 175  
Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp  
180 185 190  
Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp  
195 200 205  
Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp  
210 215 220  
Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln  
225 230 235 240  
Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu  
245 250 255  
Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr  
260 265 270  
Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp  
275 280 285  
Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala  
290 295 300  
Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala  
305 310 315 320  
Cys Ala

<210> SEQ ID NO:3  
<211> LENGTH: 74  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG474

<400> SEQ ID NO:3  
cagatggata caccctgag ccagcactgg aagttctgtt ccaggggcccg 60  
ccccagacaa accg 74

<210> SEQ ID NO:4  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide RS366

<400> SEQ ID NO:4  
acaacgcaca gaatcttagcg 20

<210> SEQ ID NO:5  
<211> LENGTH: 74  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG475

<400> SEQ ID NO:5  
cacactccca gcccacccat ccacgctgga agttctgttc caggggccct tgactcatcc 60  
tcagagacga atcg 74

<210> SEQ ID NO:6  
<211> LENGTH: 57  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG479

<400> SEQ ID NO:6  
gctcgaattc tcaatgtatgtat gggcacaggc agcctcagcc ttctgtg 57